REMARKS

Claims 1-11, 13-14, 17, 21, 24, 26-27 and 50 are currently under consideration. The claims have been amended to more particularly and distinctly claim the invention. No new mater is added.

Applicants wish to thank Examiners Steele and Tsang for the courtesy extended during the telephonic interview of June 4, 2012 in which the rejections based on Minden were discussed.

A. The Claims Are Not Obvious in View of Minden, Nelson, Kumar, Barry, Cardone or Mathew

Claims 1-11, 13-14, 21, 24 and 26-27 are rejected under 35 U.S.C. §103(a) as being unpatentable over Minden et al. WO 02/086081 A2 ("Minden") and Nelson et al. U.S. Patent 6,887,713 ("Nelson") and U.S. Patent Application Publication 2002/0110835 (published August 15, 2002; "Kumar".

Claims 1-11, 13-14, 21, 24, and 26-27 are rejected under 35 U.S.C. 103(a) as being unpatentable over Minden , Barry et al. WO 0225287 (filed September 19, 2001), and Kumar.

Claims 1-11, 13-14, 17, 21, 24, 26-27 and 50 are rejected under 35 U.S.C. 103(a) as being unpatentable over over Minden, Barry, Kumar and Cardone (US Patent Application 20020076727: "Cardone").

Claims 1-11, 13-14, 17, 21, 24, and 26-27 are rejected under 35 U.S.C. 103(a) as being unpatentable over Minden, Barry, Kumar and Mathew (US Patent Application 20030232396:"Mathew").

Applicant maintains that, for reasons detailed below, the present invention is not render obvious by Minden, Nelson, Kumar, Barry, Cardone or Mathew either alone or in combination.

The present invention is directed to the use of arrays for characterizing the proteins, peptides, protein fragments or peptide fragments in a heterogenous sample. It is essential to note that the use of such arrays allows a significant reduction in the number of antibodies utilized for analysis of samples of large numbers of proteins, peptides, protein fragments or peptide fragements (including the entire proteome). This reduction is achieved by each antibody being capable of binding multiple different proteins, peptides, protein fragments or peptide fragements that share a motif in common. The ability to bind multiple different proteins, peptides, protein

fragments or peptide fragements sharing a common motif is the essence of the invention and not how they are identified (i.e., the mass/abundance measurement step).

Applicant asserts that a key difference between the presently claimed invention and the disclosure of Minden is that the present invention does not, as in Minden, identify or characterize the proteins, peptides, protein fragments or peptide fragments by assessing the pattern of binding of a sample to the array and comparing the identified binding pattern to a reference set of binding patterns to identify the proteins. As discussed throughout Minden, the screening method involves contacting peptide fragments with an array to promote specific interactions of the fragments with the array, detecting the binding pattern of the peptide fragments on the array and comparing the binding patterns of the peptide fragments to a reference set (see paragraphs [0005] and [0039] of Minden, for example). The reference set is defined in paragraph [0031] as "a data set containing information that allows identification of a protein based on its binding pattern to a given set of binding reagents." Thus, the identification and characterization of the peptides in the sample of Minden is carried out away from the array with a comparison of binding patterns in silico. Specifically, in Minden, the characterizing of the peptides is not carried out at the defined and discrete locations on the array where individual antibodies with specificity for single motifs and hence single classes of peptide) are located.

The characterisation of the peptides in Minden is carried out indirectly with reference to multiple locations (sets) on the array indirectly by comparison of patterns of binding with patterns already generated using known proteins. This is made clear for example at Minden paragraph [0045] where it is indicated that a:

> "concurrent goal is that the minimum set produces a unique binding pattern for the peptide fragments of each protein within the mixture. Thus, in one embodiment, a solution set of binding reagents provides for identification of a maximum number of proteins within a given protein mixture using the fewest number of binding reagents possible."

Therefore, it is clear that interaction with several different binding sites is needed to produce an approximate binding pattern to enable identification.

In contrast, the present invention involves assessing the bound peptides at individual sites on the array using mass spectrometry to identify their mass and abundance; this is not carried out or suggested by Minden. As explained throughout the present specification, for example at paragraph [0016], each "class" of peptide binds to a single specific binding molecule at a defined and distinct point on the array. The characterising step is performed on proteins in each class "at

each defined and discrete location on the array" (see paragraphs [0013], [0098] and [0100], for example), and hence at each site individually. No such step is performed in the methods of Minden. Also, at no point in the presently claimed methods is there an assessment of overall binding patterns nor any comparison of binding patterns with reference binding patterns like those in Minden. Therefore, the very nature of the strategy used to identify and characterise proteins in a sample differs between Minden and the present invention.

To expedite the allowance of claims and to more clearly distinguish the presently claimed invention from Minden, Applicant has amended Claim 1 to incorporate the features of Claim 21. Claim 1 as amended recites that "characterization of the bound proteins, peptides, or protein fragments or peptide fragments, occurs at the defined and discrete locations on the array." With regard to claim 21, the Examiner maintains that paragraphs [0005], [0028]-[0031], and [0040] of Minden are of significance. Applicant respectfully disagrees. These paragraphs do not teach the feature of Claim 21. As explained above, paragraph [0005] provides an overview of the method of the invention where binding patterns are compared with a reference set; paragraphs [0028] and [0029] merely relate to the binding reagents, which is of no relevance to Claim 21; paragraph [0030] defines "solution sets" and thus clarifies that "sets" of binding sites are involved in the characterisation and not individual sites; paragraph [0031] provides a definition of "reference set", which is not relevant to the present invention; and paragraph [0040] merely describes an embodiment where it is clarified that "sets of epitopes" are involved in the characterisation.

In summary, the prior art methods, including those of Minden, require some prior knowledge of the components of a protein sample, or at least the generation of reference binding sets, in order to identify proteins in a sample. The present invention provides an effective means of identifying proteins in a sample with no prior knowledge of the components. Also, the present invention is able to detect a very large number of proteins using only relatively few binding molecules thus providing a significant advantage over the prior art.

With regard to Nelson, Kumar, Barry, Cardone and Mathew, Applicant maintains that these secondary references fail to supply the disclosure that is absent from Minden, i.e., a means for complex sample evaluation with relatively small arrays. The combined teachings of Minden and Nelson, Kumar, Barry, Cardone and Mathew are conceptually different and not interchangeable with the claimed invention and would give strikingly different end results. Hence, the claims are non-obvious over the combination of Minden, Nelson, Kumar, Barry, Cardone or Mathew therefore, the rejection under 35 U.S.C. §103 should be withdrawn.

B. References Diclosing Methods of Epitope Mapping do not Anticipate or Render Obvious the Claimed Invention

During the telephonic interview of June 4, 2012, the Examiner discussed the general state of the art regarding epitope mapping. The following three references were provided by the Examiner as evidence of that general state of the art:

(i) Rydlander et al. "Molecular Characterization of a Tissue-polypeptide-specific-Antigen Epitope and its Relationship to Human Cytokeratin 18" (1996)Eur. J. Biochem. 241:309-314;

(ii) Parker and Tomer "MALDI/MS-Based Epitope Mapping of Antigens Bound to Immobilied Antibodies" (2002) Molecular Biotechnology 20:49-62; and

(iii) Jeyararajah et al., "Matrix-Assisted Laser Desorption Ionization/Mass Spectrometry Mapping of Human Immunodeficiency virus-gp 120 Epitopes Recognized by a Limited Polyclonal Antibody" (1998) J. Am Soc. Mass Spectrom 9:157-165.

Applicant maintains that the presently claimed invention is neither anticipated, nor rendered obvious, by the above references. In each of the cited references, the goal is simply to determine the region of a target protein, i.e., epitope, that any given binder, such as an antibody, binds to. In contrast, the present invention does not involve merely determining the epitopes of proteins. Rather, the present invention uses antibodies to enrich protein or peptide samples containing the epitopes with the aim of identifying the proteins or peptides. Epitope mapping is not designed to identify the proteins in which the epitopes are located. Further, the claimed methods of the present invention are carried out on a heterogenous sample of proteins or peptides with unknown composition. In contrast, it would not be possible to carry out epitope mapping on a heterogenous sample of proteins or peptides.

Thus, the claims are not anticipated, nor obvious, over over general methods of epitope mapping.

CONCLUSION

In view of the foregoing amendments and remarks, it is believed that the subject claims are in condition for allowance, which action is earnestly solicited. If, in the opinion of the Examiner, a telephone conference would expedite prosecution of the subject application, the Examiner is invited to call the undersigned attorney.

Respectfully submitted,

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